RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: *10/622,201*
Source: *IFW16*
Date Processed by STIC: *3-15-05*

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/622,201

CRF Edit Date: 3/15/05

Edited by: _____

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

✓ Deleted: ✓ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

RAW SEQUENCE LISTING   DATE: 03/15/2005
PATENT APPLICATION: US/10/622,201   TIME: 17:01:43

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03152005\J622201.raw

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    3 <110> APPLICANT: Barry, Gerard F.
    4        Kishore, Ganesh M.
    5        Padgette, Stephen R.
    6        Stallings, William C.
    8 <120> TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
SYNTHASES
   11 <130> FILE REFERENCE: 11899.0175.REUS07
   13 <140> CURRENT APPLICATION NUMBER: 10/622,201
   14 <141> CURRENT FILING DATE: 2003-07-18
   16 <150> PRIOR APPLICATION NUMBER: US 08/306,063
   17 <151> PRIOR FILING DATE: 1994-09-13
   19 <150> PRIOR APPLICATION NUMBER: US 07/749,611
   20 <151> PRIOR FILING DATE: 1991-08-28
   22 <150> PRIOR APPLICATION NUMBER: US 07/576,537
   23 <151> PRIOR FILING DATE: 1990-08-31
   25 <160> NUMBER OF SEQ ID NOS: 70
   27 <170> SOFTWARE: PatentIn version 3.3
   29 <210> SEQ ID NO: 1
   30 <211> LENGTH: 597
   31 <212> TYPE: DNA
   32 <213> ORGANISM: Figwort mosaic virus
   34 <400> SEQUENCE: 1
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   37 actttattca aattggtatc gccaaaacca agaaggaact cccatcctca aaggtttgta     120
   39 aggaagaatt ctcagtccaa agcctcaaca aggtcagggt acagagtctc caaaccatta     180
   41 gccaaaagct acaggagatc aatgaagaat cttcaatcaa agtaaactac tgttccagca     240
   43 catgcatcat ggtcagtaag tttcagaaaa agacatccac cgaagactta aagttagtgg     300
   45 gcatctttga aagtaatctt gtcaacatcg agcagctggc ttgtggggac cagacaaaaa     360
   47 aggaatggtg cagaattgtt aggcgcacct accaaaagca tctttgcctt tattgcaaag     420
   49 ataaagcaga ttcctctagt acaagtgggg aacaaataa cgtggaaaag agctgtcctg     480
   51 acagcccact cactaatgcg tatgacgaac gcagtgacga ccacaaaaga attccctcta     540
   53 tataagaagg cattcattcc catttgaagg atcatcagat actaaccaat atttctc       597
   56 <210> SEQ ID NO: 2
   57 <211> LENGTH: 1982
   58 <212> TYPE: DNA
   59 <213> ORGANISM: Agrobacterium sp.
   62 <220> FEATURE:
   63 <221> NAME/KEY: CDS
   64 <222> LOCATION: (62)..(1426)
   66 <400> SEQUENCE: 2
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   69 c atg tcg cac ggt gca agc agc cgg ccc gca acc gcc cgc aaa tcc tct     109
   70   Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
   71   1               5                   10                  15
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(pg. 6)

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73 ggc ctt tcc gga acc gtc cgc att ccc ggc gac aag tcg atc tcc cac       157
74 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
75          20                  25                  30
77 cgg tcc ttc atg ttc ggc ggt ctc gcg agc ggt gaa acg cgc atc acc       205
78 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
79          35                  40                  45
81 ggc ctt ctg gaa ggc gag gac gtc atc aat acg ggc aag gcc atg cag       253
82 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
83      50                  55                  60
85 gcc atg ggc gcc agg atc cgt aag gaa ggc gac acc tgg atc atc gat       301
86 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
87 65                  70                  75                  80
89 ggc gtc ggc aat ggc ggc ctc ctg gcg cct gag gcg ccg ctc gat ttc       349
90 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
91                  85                  90                  95
93 ggc aat gcc gcc acg ggc tgc cgc ctg acc atg ggc ctc gtc ggg gtc       397
94 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
95                  100                 105                 110
97 tac gat ttc gac agc acc ttc atc ggc gac gcc tcg ctc aca aag cgc       445
98 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
99          115                 120                 125
101 ccg atg ggc cgc gtg ttg aac ccg ctg cgc gaa atg ggc gtg cag gtg      493
102 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
103      130                 135                 140
105 aaa tcg gaa gac ggt gac cgt ctt ccc gtt acc ttg cgc ggg ccg aag      541
106 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
107 145                 150                 155                 160
109 acg ccg acg ccg atc acc tac cgc gtg ccg atg gcc tcc gca cag gtg      589
110 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
111                 165                 170                 175
113 aag tcc gcc gtg ctg ctc gcc ggc ctc aac acg ccc ggc atc acg acg      637
114 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
115                 180                 185                 190
117 gtc atc gag ccg atc atg acg cgc gat cat acg gaa aag atg ctg cag      685
118 Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
119                 195                 200                 205
121 ggc ttt ggc gcc aac ctt acc gtc gag acg gat gcg gac ggc gtg cgc      733
122 Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
123      210                 215                 220
125 acc atc cgc ctg gaa ggc cgc ggc aag ctc acc ggc caa gtc atc gac      781
126 Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
127 225                 230                 235                 240
129 gtg ccg ggc gac ccg tcc tcg acg gcc ttc ccg ctg gtt gcg gcc ctg      829
130 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
131                 245                 250                 255
133 ctt gtt ccg ggc tcc gac gtc acc atc ctc aac gtg ctg atg aac ccc      877
134 Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
135                 260                 265                 270
137 acc cgc acc ggc ctc atc ctg acg ctg cag gaa atg ggc gcc gac atc      925
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138 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
139         275             280             285
141 gaa gtc atc aac ccg cgc ctt gcc ggc ggc gaa gac gtg gcg gac ctg      973
142 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
143         290             295             300
145 cgc gtt cgc tcc tcc acg ctg aag ggc gtc acg gtg ccg gaa gac cgc     1021
146 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
147 305             310             315             320
149 gcg cct tcg atg atc gac gaa tat ccg att ctc gct gtc gcc gcc gcc     1069
150 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
151             325             330             335
153 ttc gcg gaa ggg gcg acc gtg atg aac ggt ctg gaa gaa ctc cgc gtc     1117
154 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
155         340             345             350
157 aag gaa agc gac cgc ctc tcg gcc gtc gcc aat ggc ctc aag ctc aat     1165
158 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
159         355             360             365
161 ggc gtg gat tgc gat gag ggc gag acg tcg ctc gtc gtg cgc ggc cgc     1213
162 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
163         370             375             380
165 cct gac ggc aag ggg ctc ggc aac gcc tcg ggc gcc gcc gtc gcc acc     1261
166 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
167 385             390             395             400
169 cat ctc gat cac cgc atc gcc atg agc ttc ctc gtc atg ggc ctc gtg     1309
170 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
171             405             410             415
173 tcg gaa aac cct gtc acg gtg gac gat gcc acg atg atc gcc acg agc     1357
174 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
175         420             425             430
177 ttc ccg gag ttc atg gac ctg atg gcc ggg ctg ggc gcg aag atc gaa     1405
178 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
179         435             440             445
181 ctc tcc gat acg aag gct gcc tgatgacctt cacaatcgcc atcgatggtc         1456
182 Leu Ser Asp Thr Lys Ala Ala
183     450             455
185 ccgctgcggc cggcaagggg acgctctcgc gccgtatcgc ggaggtctat ggctttcatc    1516
187 atctcgatac gggcctgacc tatcgcgcca cggccaaagc gctgctcgat cgcggcctgt    1576
189 cgcttgatga cgaggcggtt gcggccgatg tcgcccgcaa tctcgatctt gccgggctcg    1636
191 accggtcggt gctgtcggcc catgccatcg gcgaggcggc ttcgaagatc gcggtcatgc    1696
193 cctcggtgcg gcgggcgctg gtcgaggcgc agcgcagctt gcggcgcgt gagccgggca     1756
195 cggtgctgga tggacgcgat atcggcacgg tggtctgccc ggatgcgccg gtgaagctct    1816
197 atgtcaccgc gtcaccggaa gtgcgcgcga aacgccgcta tgacgaaatc ctcggcaatg    1876
199 gcgggttggc cgattacggg acgatcctcg aggatatccg ccgccgcgac gagcgggaca    1936
201 tgggtcgggc ggacagtcct ttgaagcccg ccgacgatgc gcactt                   1982
204 <210> SEQ ID NO: 3
205 <211> LENGTH: 455
206 <212> TYPE: PRT
207 <213> ORGANISM: Agrobacterium sp.
209 <400> SEQUENCE: 3
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215 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
216             20                  25              30
219 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
220         35                  40              45
223 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
224     50                  55              60
227 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
228 65                  70                  75              80
231 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
232             85                  90              95
235 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
236             100                 105             110
239 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
240         115                 120             125
243 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
244     130                 135             140
247 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
248 145                 150                 155             160
251 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
252             165                 170             175
255 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
256             180                 185             190
259 Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
260         195                 200             205
263 Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
264     210                 215             220
267 Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
268 225                 230                 235             240
271 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
272             245                 250             255
275 Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
276             260                 265             270
279 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
280         275                 280             285
283 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
284     290                 295             300
287 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
288 305                 310                 315             320
291 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
292             325                 330             335
295 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
296             340                 345             350
299 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
300         355                 360             365
303 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
304     370                 375             380
307 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
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RAW SEQUENCE LISTING   DATE: 03/15/2005
PATENT APPLICATION: US/10/622,201   TIME: 17:01:43

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03152005\J622201.raw**

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311 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
312             405                  410                  415
315 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
316             420                  425                  430
319 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
320         435                  440                  445
323 Leu Ser Asp Thr Lys Ala Ala
324     450                  455
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 1673
329 <212> TYPE: DNA
330 <213> ORGANISM: Agrobacterium sp.
333 <220> FEATURE:
334 <221> NAME/KEY: CDS
335 <222> LOCATION: (86)..(1432)
337 <400> SEQUENCE: 4
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340 gccaaaatgt gactgtgaaa aatcc atg tcc cat tct gca tcc ccg aaa cca       112
341                            Met Ser His Ser Ala Ser Pro Lys Pro
342                            1               5
344 gca acc gcc cgc cgc tcg gag gca ctc acg ggc gaa atc cgc att ccg       160
345 Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
346 10                  15                  20                  25
348 ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca       208
349 Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
350             30                  35                  40
352 tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac gtc atc       256
353 Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
354             45                  50                  55
356 aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt aaa gag       304
357 Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
358         60                  65                  70
360 ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg ttg cag       352
361 Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
362     75                  80                  85
364 ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg cgc ctc       400
365 Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
366 90                  95                  100                 105
368 acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt atc ggc       448
369 Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly
370             110                 115                 120
372 gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac ccg ttg       496
373 Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu
374             125                 130                 135
376 cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc atg ccg       544
377 Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro
378         140                 145                 150
380 ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat cgc gtg       592
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RAW SEQUENCE LISTING   DATE: 03/15/2005
PATENT APPLICATION: US/10/622,201   TIME: 17:01:43

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03152005\J622201.raw**

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308 385                  390                  395                  400
311 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
312             405                  410                  415
315 Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
316             420                  425                  430
319 Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
320         435                  440                  445
323 Leu Ser Asp Thr Lys Ala Ala
324     450                  455
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 1673
329 <212> TYPE: DNA
330 <213> ORGANISM: Agrobacterium sp.
333 <220> FEATURE:
334 <221> NAME/KEY: CDS
335 <222> LOCATION: (86)..(1432)
337 <400> SEQUENCE: 4
338 gtagccacac ataattacta tagctaggaa gcccgctatc tctcaatccc gcgtgatcgc      60
340 gccaaaatgt gactgtgaaa aatcc atg tcc cat tct gca tcc ccg aaa cca       112
341                            Met Ser His Ser Ala Ser Pro Lys Pro
342                            1               5
344 gca acc gcc cgc cgc tcg gag gca ctc acg ggc gaa atc cgc att ccg       160
345 Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
346 10                  15                  20                  25
348 ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca       208
349 Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
350             30                  35                  40
352 tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac gtc atc       256
353 Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
354             45                  50                  55
356 aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt aaa gag       304
357 Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
358         60                  65                  70
360 ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg ttg cag       352
361 Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
362     75                  80                  85
364 ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg cgc ctc       400
365 Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
366 90                  95                  100                 105
368 acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt atc ggc       448
369 Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly
370             110                 115                 120
372 gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac ccg ttg       496
373 Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu
374             125                 130                 135
376 cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc atg ccg       544
377 Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro
378         140                 145                 150
380 ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat cgc gtg       592
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/15/2005
PATENT APPLICATION: **US/10/622,201**   TIME: 17:01:44

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03152005\J622201.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; Xaa Pos. 1,18
Seq#:22; N Pos. 9
Seq#:23; N Pos. 9
Seq#:30; Xaa Pos. 1
Seq#:37; Xaa Pos. 2,4
Seq#:38; Xaa Pos. 4
Seq#:39; Xaa Pos. 4
Seq#:40; Xaa Pos. 2
Seq#:54; Xaa Pos. 8

VERIFICATION SUMMARY   DATE: 03/15/2005
PATENT APPLICATION: **US/10/622,201**   TIME: 17:01:44

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03152005\J622201.raw**

L:1307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
M:341 Repeated in SeqNo=18
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:1476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:1605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:1626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:1647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:2789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0

IFW16

```
 3 <110> APPLICANT: Barry, Gerard F.
 4         Kishore, Ganesh M.
 5         Padgette, Stephen R.
 6         Stallings, William C.
 8 <120> TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
SYNTHASES
11 <130> FILE REFERENCE: 11899.0175.REUS07
13 <140> CURRENT APPLICATION NUMBER: 10/622,201
14 <141> CURRENT FILING DATE: 2003-07-18
16 <150> PRIOR APPLICATION NUMBER: US 08/306,063
17 <151> PRIOR FILING DATE: 1994-09-13
19 <150> PRIOR APPLICATION NUMBER: US 07/749,611
20 <151> PRIOR FILING DATE: 1991-08-28
22 <150> PRIOR APPLICATION NUMBER: US 07/576,537
23 <151> PRIOR FILING DATE: 1990-08-31
25 <160> NUMBER OF SEQ ID NOS: 70
27 <170> SOFTWARE: PatentIn version 3.3
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Does Not Comply
Corrected Diskette Needed
(pg. 2-5)

ERRORED SEQUENCES

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4579 <210> SEQ ID NO: 69
4580 <211> LENGTH: 443
4581 <212> TYPE: PRT
4582 <213> ORGANISM: Dichelobacter nodosus
4584 <400> SEQUENCE: 69
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4591             20                  25                  30
4594 Leu Ala Ala Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala
4595         35                  40                  45
4598 Cys Ala Asp Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val
4599     50                  55                  60
4602 Asp Ile Gln Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe
4603 65                  70                  75                  80
4606 Leu Gly Leu Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly
4607             85                  90                  95
4610 Thr Ser Met Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu
4611             100                 105                 110
4614 Ser Val Leu Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg
4615             115                 120                 125
4618 Ile Ile Thr Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser
4619         130                 135                 140
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RAW SEQUENCE LISTING   DATE: 03/10/2005
PATENT APPLICATION: **US/10/622,201**   TIME: 15:45:20

Input Set : **A:\11899.0175.REUS07.ST25.txt**
Output Set: **N:\CRF4\03102005\J622201.raw**

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4623 145             150             155             160
4626 Asp Tyr Ala Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile
4627             165             170             175
4630 Leu Ala Gly Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly
4631             180             185             190
4634 Ile Ser Arg Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala
4635             195             200             205
4638 Leu Glu Ile Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu
4639     210             215             220
4642 His Gly Cys Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe
4643 225             230             235             240
4646 Phe Met Val Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg
4647             245             250             255
4650 Asn Val Gly Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln
4651             260             265             270
4654 Lys Met Gly Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala
4655             275             280             285
4658 Glu Pro Val Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile
4659     290             295             300
4662 Thr Val Ala Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile
4663 305             310             315             320
4666 Phe Phe Ile Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn
4667             325             330             335
4670 Leu Ser Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala
4671             340             345             350
4674 Gln Asn Leu Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe
4675             355             360             365
4678 Ile His Ile Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val
4679     370             375             380
4682 Asn Ser Phe Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly
4683 385             390             395             400
4686 Val Arg Ala Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala
4687             405             410             415
4690 Val Ser Met Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn
4691             420             425             430
4694 Val Gly Glu Lys Asp Ala Lys Asn Cys His Asp
4695             435             440
```

E--> **4697**

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    4698 <210> SEQ ID NO: 70
    4699 <211> LENGTH: 455
    4700 <212> TYPE: PRT
    4701 <213> ORGANISM: Artificial sequence
    4703 <220> FEATURE:
    4704 <223> OTHER INFORMATION: Synthetic
    4706 <400> SEQUENCE: 70
    4708 Met Leu His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
    4709 1             5             10             15
    4712 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
```

see page 5 for error explanation.

```
4713              20                    25                    30
4716 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
4717         35                    40                    45
4720 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
4721         50                    55                    60
4724 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
4725 65                    70                    75                    80
4728 Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
4729              85                    90                    95
4732 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
4733         100                   105                   110
4736 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
4737         115                   120                   125
4740 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
4741         130                   135                   140
4744 Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
4745 145                   150                   155                   160
4748 Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
4749              165                   170                   175
4752 Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
4753         180                   185                   190
4756 Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
4757         195                   200                   205
4760 Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
4761         210                   215                   220
4764 Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
4765 225                   230                   235                   240
4768 Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
4769              245                   250                   255
4772 Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
4773         260                   265                   270
4776 Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
4777         275                   280                   285
4780 Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
4781         290                   295                   300
4784 Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
4785 305                   310                   315                   320
4788 Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
4789              325                   330                   335
4792 Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
4793         340                   345                   350
4796 Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
4797         355                   360                   365
4800 Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
4801         370                   375                   380
4804 Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
4805 385                   390                   395                   400
4808 His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
4809              405                   410                   415
```

See pages 5 for error explanation

RAW SEQUENCE LISTING   DATE: 03/10/2005

PATENT APPLICATION: US/10/622,201   TIME: 15:45:20

Input Set : A:\11899.0175.REUS07.ST25.txt

Output Set: N:\CRF4\03102005\J622201.raw

4812	Ser	Glu	Asn	Pro	Val	Thr	Val	Asp	Asp	Ala	Thr	Met	Ile	Ala	Thr	Ser
4813				420					425					430		
4816	Phe	Pro	Glu	Phe	Met	Asp	Leu	Met	Ala	Gly	Leu	Gly	Ala	Lys	Ile	Glu
4817			435					440					445			
4820	Leu	Ser	Asp	Thr	Lys	Ala	Ala									
4821		450				455										

E--> 4824

see page 5 for error explanation, (handwritten)

<U> deleted

<210>   70
<211>   455
<212>   PRT
<213>   Artificial sequence

<220>
<223>   Synthetic

<400>   70

```
Met Leu His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
1               5                   10                  15

Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
            20                  25                  30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
            35              40                  45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
        50              55                  60

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65                  70                  75                  80

Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
                85                  90                  95

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
            100                 105                 110

Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
        115                 120                 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
    130                 135                 140

Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
145                 150                 155                 160

Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
                165                 170                 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
            180                 185                 190
```

VERIFICATION SUMMARY   DATE: 03/10/2005
PATENT APPLICATION: **US/10/622,201**   TIME: 15:45:21

Input Set : **A:\11899.0175.REUS07.ST25.txt**
Output Set: **N:\CRF4\03102005\J622201.raw**

```
L:1307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
M:341 Repeated in SeqNo=18
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:1476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:1605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:1626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:1647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:2789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:4697 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:4697 M:252 E: No. of Seq. differs, <211> LENGTH:Input:443 Found:444 SEQ:69
L:4824 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:4824 M:252 E: No. of Seq. differs, <211> LENGTH:Input:455 Found:456 SEQ:70
```